REMARKS

Applicant hereby submits that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely insert the paper copy of the Sequence Listing and sequence identifiers in the specification, and replace the informal drawings with formal drawings. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket number 12125-002001.

Respectfully submitted,

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"Version With Markings to Show Changes Made"

In the specification:

Paragraph beginning at page 6, line 4, has been amended as follows:

[Fig. 2 is] Figs. 2A-2B are a set of diagrams that depict the characteristics of long discordant helix segments. Amino acid sequences, together with determined and predicted secondary structure elements for sequences having ≥9=residue discordant segments are shown. Also shown are those discordant segments of Aβ, mouse PrP, and human PrP. The proteins are grouped by the length of their discordant stretch. The experimentally determined helical segments are drawn as blue cylinders in the bottom row of each case in which the amino acid sequences and residue positions in the PDB entries of the corresponding proteins are given (Top to bottom in each set: Set 16 contains SEQ ID NOs:4-6; Set 15 contains SEQ ID NOs:7 and 8; Set 8 contains SEQ ID NO:9; Set 13 contains SEQ ID NOs:10 and 11; Set 12 contains SEQ ID NOs:12 and 13; Set 10 contains SEQ ID NOs:14 and 15; Set 11 contains SEQ ID NOs:16-18; Set 9 contains SEQ ID NOs:19-20 (top row left to right) and 21-23 (bottom row left to right). The locations of the β-strands predicted by PHD are visualized by yellow strands in the middle row of each case, wherein the reliability index for each residue is shown. The Chou-Fasman-based predictions averaged for 6-residue segments are plotted above residue 3 in each segment and given in the top row of each case. E and e denote extended structures (i.e., β-strands) predicted with high and low probability, respectively, as in Chou and Fasman (1978, Adv. Enzymol. 47:45-148), and H and h represent predicted helical structures in an analogous manner.

Paragraph beginning at page 6, line 18, has been amended as follows:

Fig. 3 is a diagram that depicts the amino acid sequence (bottom row; SEQ ID NO:24) and predicted secondary structure by PHD and according to Chou-Fasman analysis for a polyleucine analogue of SP-C (lung surfactant protein C). The PHD predictions including reliability indices are given in the middle row and the Chou-Fasman data in the top row, but in this case an α-helix is predicted by both methods, symbolized by a blue cylinder for the PHD prediction.

Paragraph beginning at page 6, line 27, has been amended as follows:

Fig. 5 is a set of diagrams that depict the experimentally determined and predicted secondary structures of positions 1-28 of Aβ (SEQ ID NO:25; top) and a variant of Aβ (1-28) in which three residues have been changed to alanine (K16A, L17A, F20A) (SEQ ID NO:26; bottom). Symbols are as described for Figs. 2 and 4.